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#2 OIPE

RAW SEQUENCE LISTING   DATE: 04/05/2001
PATENT APPLICATION: US/09/813,329   TIME: 12:43:12

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Output Set: N:\CRF3\04052001\I813329.raw

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 3 <110> APPLICANT: Bristol-Myers Suibb Company
 5 <120> TITLE OF INVENTION: Novel Drosophila Tumor Necrosis Factor Class Molecule ("DmTNF") and
 6       Variants Thereof
 8 <130> FILE REFERENCE: D0016.np
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/813,329
C--> 10 <141> CURRENT FILING DATE: 2001-03-20
10 <150> PRIOR APPLICATION NUMBER: 60/190,816
11 <151> PRIOR FILING DATE: 2000-03-21
13 <160> NUMBER OF SEQ ID NOS: 65
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2166
19 <212> TYPE: DNA
20 <213> ORGANISM: Drosophila melanogastor
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (652)..(1878)
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29 taaatcagag atcccaagca agcgcgtgcg tgcatgatag cgaagaaaaa aagctatccg     120
31 tttcagttaa ctacttacca agattgaatt tcgccatcgg gcaaattact aaaaatacat     180
33 aagtgcaact cgtccactgt gtgttgtgtt tttttttttt tttttggttt tcgctgtgcc     240
35 tttatcgcaa acaagaactg ataaaactag aaaatatctt gagaaacttg ttttcgcgct     300
37 tttcttttgc taattgccga tcgcggaaga gaaaaacaag cagtagacaa aacaagtgtg     360
39 gtaatacaat ctgaaaaggg caccatcagc agcccgaggg gtttatctat atagatgtcg     420
41 cagcttatca tctcatgctg tctgtgaggt tgttctgtgt gctcgtgtag tatcttaaat     480
43 acatagagtg tgttcatata aagtgcgaca aagctcgatt ggaaacagct gtcgagtgcc     540
45 cttgagtggg tgggcaagat cgtcatcatc atcatcgtcg tcattatcaa cagaatcagc     600
47 atcagcatct ggaggccccg gatgctctaa gatccccagt gttcatcaat t atg act     657
48                                                         Met Thr
49                                                           1
51 gcc gag acc ctc aag ccg ttt ata acg cca acg agt gcc aac gat gat     705
52 Ala Glu Thr Leu Lys Pro Phe Ile Thr Pro Thr Ser Ala Asn Asp Asp
53          5                   10                  15
55 ggt ttt ccg gcc aaa gcg acc agc acg gcg acc gcc cag cga cgc acc     753
56 Gly Phe Pro Ala Lys Ala Thr Ser Thr Ala Thr Ala Gln Arg Arg Thr
57      20                  25                  30
59 cgc cag ctg atc ccc ctg gtt ttg ggg ttc atc ggt ctg ggg ctg gtc     801
60 Arg Gln Leu Ile Pro Leu Val Leu Gly Phe Ile Gly Leu Gly Leu Val
61 35                  40                  45                  50
63 gtt gcc att ctc gca cta acg atc tgg cag aca acg cgt gta tcg cat     849
64 Val Ala Ile Leu Ala Leu Thr Ile Trp Gln Thr Thr Arg Val Ser His
65              55                  60                  65
67 ctg gac aag gag ctg aag agc ctg aag cga gtc gtc gat aat ctc cag     897
68 Leu Asp Lys Glu Leu Lys Ser Leu Lys Arg Val Val Asp Asn Leu Gln
69          70                  75                  80
71 cag cgt ttg ggc ata aac tat ctg gac gag ttc gac gag ttc caa aag     945
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72 Gln Arg Leu Gly Ile Asn Tyr Leu Asp Glu Phe Asp Glu Phe Gln Lys
73       85              90                 95
75 gag tac gag aat gcc ctc atc gac tat cca aaa aag gtg gat ggc ctc      993
76 Glu Tyr Glu Asn Ala Leu Ile Asp Tyr Pro Lys Lys Val Asp Gly Leu
77     100             105              110
79 acg gat gag gag gac gac gac gat ggc gat ggt ctg gat tcc att gcg      1041
80 Thr Asp Glu Glu Asp Asp Asp Asp Gly Asp Gly Leu Asp Ser Ile Ala
81 115             120              125              130
83 gac gac gag gac gac gac gtt agc tat agc tct gtg gat gat gtt ggc      1089
84 Asp Asp Glu Asp Asp Asp Val Ser Tyr Ser Ser Val Asp Asp Val Gly
85             135              140              145
87 gca gac tac gag gac tac acc gat atg tta aat aaa ctc aac aat gca      1137
88 Ala Asp Tyr Glu Asp Tyr Thr Asp Met Leu Asn Lys Leu Asn Asn Ala
89             150              155              160
91 cat acc ggc acc acg ccc aca tct gag acc act gct gag ggc gag ggc      1185
92 His Thr Gly Thr Thr Pro Thr Ser Glu Thr Thr Ala Glu Gly Glu Gly
93             165              170              175
95 gag acg gac agt gca tcc tca gcc tca aat gat gac aat gtg ttc gat      1233
96 Glu Thr Asp Ser Ala Ser Ser Ala Ser Asn Asp Asp Asn Val Phe Asp
97     180              185              190
99 gac ttt acc agc tca gat gcc ctc aaa aag aag cag gag aga aaa tct      1281
100 Asp Phe Thr Ser Ser Asp Ala Leu Lys Lys Lys Gln Glu Arg Lys Ser
101 195              200              205              210
103 cgc tcg att gcc gat gta cgc aat gag gag cag aat att caa gga aat     1329
104 Arg Ser Ile Ala Asp Val Arg Asn Glu Glu Gln Asn Ile Gln Gly Asn
105             215              220              225
107 cac aca gag ctt cag gaa aag tca tcc aat gag gca gct tcc aaa gag     1377
108 His Thr Glu Leu Gln Glu Lys Ser Ser Asn Glu Ala Ala Ser Lys Glu
109             230              235              240
111 agc cct gca gca ctt cac ctc cgt cgc aga atg cat tcc cgc cat cgc     1425
112 Ser Pro Ala Ala Leu His Leu Arg Arg Arg Met His Ser Arg His Arg
113         245              250              255
115 cac ctc gta gtc cgc aaa gcc aga tcc gag gac tcg agg cca gca gcc     1473
116 His Leu Val Val Arg Lys Ala Arg Ser Glu Asp Ser Arg Pro Ala Ala
117     260              265              270
119 cat ttc cac ttg agc agc agg cgg cgt cac caa gaa agt atg ggc tac     1521
120 His Phe His Leu Ser Ser Arg Arg Arg His Gln Glu Ser Met Gly Tyr
121 275              280              285              290
123 cat gga gat atg tac ata gaa aat gat agg gag aga tgc tct tat cag     1569
124 His Gly Asp Met Tyr Ile Glu Asn Asp Arg Glu Arg Cys Ser Tyr Gln
125             295              300              305
127 gga cac ttt caa acg cgc gat ggc gta ttg acg gtg acc aat gca ggc     1617
128 Gly His Phe Gln Thr Arg Asp Gly Val Leu Thr Val Thr Asn Ala Gly
129             310              315              320
131 cta tat tac gta tac gcc cag ata tgg ggc tac aac tcg cac gac cag     1665
132 Leu Tyr Tyr Val Tyr Ala Gln Ile Trp Gly Tyr Asn Ser His Asp Gln
133         325              330              335
135 aac gga ttt atc gtc ttt caa gga gac act cca ttc ctg cag tgc ttg     1713
136 Asn Gly Phe Ile Val Phe Gln Gly Asp Thr Pro Phe Leu Gln Cys Leu
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137    340                345                350
139 aac acg gtg ccc acc aac atg cca cat aag gtg cac acc tgc cac acg    1761
140 Asn Thr Val Pro Thr Asn Met Pro His Lys Val His Thr Cys His Thr
141 355              360                365                370
143 agt ggt ctg atc cac ctg gaa cga aac gag agg atc cat ctg aag gac    1809
144 Ser Gly Leu Ile His Leu Glu Arg Asn Glu Arg Ile His Leu Lys Asp
145              375                380                385
147 att cac aac gat cgc aat gca gtt ctg cgg gag gga aac aac cga agc    1857
148 Ile His Asn Asp Arg Asn Ala Val Leu Arg Glu Gly Asn Asn Arg Ser
149              390                395                400
151 tac ttt ggc atc ttc aag gtg taaattggag agattatccc cggtcagaag       1908
152 Tyr Phe Gly Ile Phe Lys Val
153         405
155 atggaatacc agtttaagct tttgtccccg cgactgctcg tgaatgcgat tcatcgccag   1968
157 cgtgaatcca ttagttcgta gtacctagtc ttagtcactc caaacctaat ctcaatcgga   2028
159 atcgtgcata ctgcattagt cagaagacgg aggaaaatca tatttatttt gtatatactc   2088
161 gttcgactct aaaaagtgaa taaaaatata tgtagctatt aaaaaaaaaa aaaaaaaaaa   2148
163 aaaaaaaaaa acctcgag                                                 2166
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 409
168 <212> TYPE: PRT
169 <213> ORGANISM: Drosophila melanogastor
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174 1               5                 10                15
177 Asp Asp Gly Phe Pro Ala Lys Ala Thr Ser Thr Ala Thr Ala Gln Arg
178             20                25                30
181 Arg Thr Arg Gln Leu Ile Pro Leu Val Leu Gly Phe Ile Gly Leu Gly
182         35                40                45
185 Leu Val Val Ala Ile Leu Ala Leu Thr Ile Trp Gln Thr Thr Arg Val
186     50                55                60
189 Ser His Leu Asp Lys Glu Leu Lys Ser Leu Lys Arg Val Val Asp Asn
190 65              70                75                80
193 Leu Gln Gln Arg Leu Gly Ile Asn Tyr Leu Asp Glu Phe Asp Glu Phe
194             85                90                95
197 Gln Lys Glu Tyr Glu Asn Ala Leu Ile Asp Tyr Pro Lys Lys Val Asp
198             100               105               110
201 Gly Leu Thr Asp Glu Glu Asp Asp Asp Gly Asp Gly Leu Asp Ser
202         115               120               125
205 Ile Ala Asp Asp Glu Asp Asp Asp Val Ser Tyr Ser Ser Val Asp Asp
206     130               135               140
209 Val Gly Ala Asp Tyr Glu Asp Tyr Thr Asp Met Leu Asn Lys Leu Asn
210 145               150               155               160
213 Asn Ala His Thr Gly Thr Thr Pro Thr Ser Glu Thr Thr Ala Glu Gly
214             165               170               175
217 Glu Gly Glu Thr Asp Ser Ala Ser Ser Ala Ser Asn Asp Asp Asn Val
218             180               185               190
221 Phe Asp Asp Phe Thr Ser Ser Asp Ala Leu Lys Lys Lys Gln Glu Arg
222         195               200               205
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225 Lys Ser Arg Ser Ile Ala Asp Val Arg Asn Glu Glu Gln Asn Ile Gln
226     210             215             220
229 Gly Asn His Thr Glu Leu Gln Glu Lys Ser Ser Asn Glu Ala Ala Ser
230 225             230             235             240
233 Lys Glu Ser Pro Ala Ala Leu His Leu Arg Arg Arg Met His Ser Arg
234             245             250             255
237 His Arg His Leu Val Val Arg Lys Ala Arg Ser Glu Asp Ser Arg Pro
238             260             265             270
241 Ala Ala His Phe His Leu Ser Ser Arg Arg Arg His Gln Glu Ser Met
242         275             280             285
245 Gly Tyr His Gly Asp Met Tyr Ile Glu Asn Asp Arg Glu Arg Cys Ser
246     290             295             300
249 Tyr Gln Gly His Phe Gln Thr Arg Asp Gly Val Leu Thr Val Thr Asn
250 305             310             315             320
253 Ala Gly Leu Tyr Tyr Val Tyr Ala Gln Ile Trp Gly Tyr Asn Ser His
254             325             330             335
257 Asp Gln Asn Gly Phe Ile Val Phe Gln Gly Asp Thr Pro Phe Leu Gln
258             340             345             350
261 Cys Leu Asn Thr Val Pro Thr Asn Met Pro His Lys Val His Thr Cys
262     355             360             365
265 His Thr Ser Gly Leu Ile His Leu Glu Arg Asn Glu Arg Ile His Leu
266     370             375             380
269 Lys Asp Ile His Asn Asp Arg Asn Ala Val Leu Arg Glu Gly Asn Asn
270 385             390             395             400
273 Arg Ser Tyr Phe Gly Ile Phe Lys Val
274             405
277 <210> SEQ ID NO: 3
278 <211> LENGTH: 1221
279 <212> TYPE: DNA
280 <213> ORGANISM: Drosophila melanogastor
282 <220> FEATURE:
283 <221> NAME/KEY: CDS
284 <222> LOCATION: (1)..(1218)
286 <400> SEQUENCE: 3
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288 Met Thr Ala Glu Thr Leu Lys Pro Phe Ile Thr Pro Thr Ser Ala Asn
289 1             5             10             15
291 gat gat ggt ttt ccg gcc aaa gcg acc agc acg gcg acc gcc cag cga     96
292 Asp Asp Gly Phe Pro Ala Lys Ala Thr Ser Thr Ala Thr Ala Gln Arg
293             20             25             30
295 cgc acc cgc cag ctg atc ccc ctg gtt ttg ggg ttc atc ggt ctg ggg    144
296 Arg Thr Arg Gln Leu Ile Pro Leu Val Leu Gly Phe Ile Gly Leu Gly
297         35             40             45
299 ctg gtc gtt gcc att ctc gca cta acg atc tgg cag aca acg cgt gta    192
300 Leu Val Val Ala Ile Leu Ala Leu Thr Ile Trp Gln Thr Thr Arg Val
301     50             55             60
303 tcg cat ctg gac aag gag ctg aag agc ctg aag cga gtc gtc gat aat    240
304 Ser His Leu Asp Lys Glu Leu Lys Ser Leu Lys Arg Val Val Asp Asn
305 65             70             75             80
```

```
307 ctc cag cag cgt ttg ggc ata aac tat ctg gac gag ttc gac gag ttc        288
308 Leu Gln Gln Arg Leu Gly Ile Asn Tyr Leu Asp Glu Phe Asp Glu Phe
309                     85                  90                  95
311 caa aag gag tac gag aat gcc ctc atc gac tat cca aaa aag gtg gat        336
312 Gln Lys Glu Tyr Glu Asn Ala Leu Ile Asp Tyr Pro Lys Lys Val Asp
313              100                 105                 110
315 ggc ctc acg gat gag gag gac gac gac gat ggc gat ggt ctg gat tcc        384
316 Gly Leu Thr Asp Glu Glu Asp Asp Asp Gly Asp Gly Leu Asp Ser
317          115                 120                 125
319 att gcg gac gac gag gac gac gac gtt agc tat agc tct gtg gat gat        432
320 Ile Ala Asp Asp Glu Asp Asp Asp Val Ser Tyr Ser Ser Val Asp Asp
321      130                 135                 140
323 gtt ggc gca gac tac gag gac tac acc gat atg tta aat aaa ctc aac        480
324 Val Gly Ala Asp Tyr Glu Asp Tyr Thr Asp Met Leu Asn Lys Leu Asn
325 145                 150                 155                 160
327 aat gca cat acc ggc acc acg ccc aca tct gag acc act gct gag ggc        528
328 Asn Ala His Thr Gly Thr Thr Pro Thr Ser Glu Thr Thr Ala Glu Gly
329                  165                 170                 175
331 gag ggc gag acg gac agt gca tcc tca gcc tca aat gat gac aat gtg        576
332 Glu Gly Glu Thr Asp Ser Ala Ser Ser Ala Ser Asn Asp Asp Asn Val
333              180                 185                 190
335 ttc gat gac ttt acc agc tac aat gcc cac aaa aag aag cag gag aga        624
336 Phe Asp Asp Phe Thr Ser Tyr Asn Ala His Lys Lys Lys Gln Glu Arg
337          195                 200                 205
339 aaa tct cgc tcg att gcc gat gta cgc aat gag gag cag aat att caa        672
340 Lys Ser Arg Ser Ile Ala Asp Val Arg Asn Glu Glu Gln Asn Ile Gln
341      210                 215                 220
343 gga aat cac aca gag ctt cag gaa aag tca tcc aat gag gca act tcc        720
344 Gly Asn His Thr Glu Leu Gln Glu Lys Ser Ser Asn Glu Ala Thr Ser
345 225                 230                 235                 240
347 aaa gag aga atg cat tcc cgc cat cgc cac ctc cta gtc cgc aaa ggt        768
348 Lys Glu Arg Met His Ser Arg His Arg His Leu Leu Val Arg Lys Gly
349                  245                 250                 255
351 gaa tct ctt ctt tca gcc aga tcc gag gac tcg agg cca gca gcc cat        816
352 Glu Ser Leu Leu Ser Ala Arg Ser Glu Asp Ser Arg Pro Ala Ala His
353              260                 265                 270
355 ttc cac ttg agc agc agg cgg cgt cac caa gga agt atg ggc tac cat        864
356 Phe His Leu Ser Ser Arg Arg Arg His Gln Gly Ser Met Gly Tyr His
357          275                 280                 285
359 gga gat atg tac ata gga aat gat aac gag aga aac tct tat cag gga        912
360 Gly Asp Met Tyr Ile Gly Asn Asp Asn Glu Arg Asn Ser Tyr Gln Gly
361      290                 295                 300
363 cac ttt caa acg cgc gat ggc gtc ttg acg gtg acc aat aca ggc cta        960
364 His Phe Gln Thr Arg Asp Gly Val Leu Thr Val Thr Asn Thr Gly Leu
365 305                 310                 315                 320
367 tat tac gta tac gcc cag ata tgc tac aac aac tcg cac gac cag aac        1008
368 Tyr Tyr Val Tyr Ala Gln Ile Cys Tyr Asn Asn Ser His Asp Gln Asn
369                  325                 330                 335
371 gga ttt atc gtc ttt caa gga gac act cca ttc ctg cag tgc ttg aac        1056
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                VERIFICATION SUMMARY              DATE: 04/05/2001
               PATENT APPLICATION:   US/09/813,329   TIME: 12:43:13

                 Input Set : A:\PTO.txt
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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